SEQUENCE LISTING

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<110>  KOBAYASHI, KAZUO
       KITAGAWA, YOSHINORI
       KOMEDA, TOSHIHIRO
       KAWASHIMA, NAGAKO
       JIGAMI, YOSHIFUMI
       CHIBA, YASUNORI

<120>  METHYLOTROPH PRODUCING MAMMALIAN TYPE SUGAR CHAIN

<130>  081356-0224

<140>  10/511,436
<141>  2004-10-25

<150>  PCT/JP03/05464
<151>  2003-04-28

<150>  JP 2002-127677
<151>  2002-04-26

<160>  121

<170>  PatentIn Ver. 3.3

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<212> PRT
<213> Ogataea minuta

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Val Leu Arg Ile Ala Leu Ser Arg Lys Asp Ile Asn Val Val Ala Val
             20                  25                  30

Asn Asp Pro Phe Ile Ala Ala Glu Tyr Ala Ala Tyr Met Phe Lys Tyr
          35                  40                  45

Asp Ser Thr His Gly Arg Tyr Gln Gly Glu Val Thr Phe Glu Gly Lys
       50                  55                  60

Tyr Leu Val Ile Asp Gly Gln Lys Ile Glu Val Phe Gln Glu Arg Asp
 65                  70                  75                  80

Pro Ala Asp Ile Pro Trp Gly Lys Glu Gly Val Asp Phe Val Ile Asp
                85                  90                  95

Ser Thr Gly Val Phe Thr Thr Thr Ala Gly Ala Gln Lys His Ile Asp
             100                 105                 110

Ala Gly Ala Lys Lys Val Ile Ile Thr Ala Pro Ser Ala Asp Ala Pro
         115                 120                 125

Met Phe Val Met Gly Val Asn His Lys Glu Tyr Thr Lys Asp Leu Ser
     130                 135                 140

Ile Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala
145                 150                 155                 160

Lys Val Val Asn Asp Val Phe Gly Ile Glu Ser Gly Leu Met Thr Thr
                 165                 170                 175

Val His Ser Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His
             180                 185                 190

Lys Asp Trp Arg Gly Gly Arg Thr Ala Ser Gly Asn Ile Ile Pro Ser
         195                 200                 205

Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Leu Pro Ala Leu Ala
     210                 215                 220

Gly Lys Leu Thr Gly Met Ser Leu Arg Val Pro Thr Thr Asp Val Ser
225                 230                 235                 240

Val Val Asp Leu Thr Val Asn Leu Lys Thr Pro Thr Thr Tyr Ala Glu
                 245                 250                 255
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Ile Ser Ala Ala Ile Lys Lys Ala Ser Glu Gly Glu Leu Ala Gly Ile
        260             265             270

Leu Gly Tyr Thr Glu Asp Ala Val Val Ser Thr Asp Phe Leu Thr Asp
        275             280             285

Asn Arg Ser Ser Ile Phe Asp Ala Ser Ala Gly Ile Leu Leu Thr Pro
    290             295             300

Thr Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser
305             310             315             320

Thr Arg Val Val Asp Leu Leu Glu His Val Ala Lys Val Ser Ser Ala
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<212> DNA
<213> Ogataea minuta

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<210> 8
<211> 524
<212> DNA
<213> Ogataea minuta

<400> 8
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<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     primer for production of an expression cassette
     with GAP gene promoter and terminator from
     Ogataea minuta

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<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
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     with GAP gene promoter and terminator from
     Ogataea minuta

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<210> 11
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 11
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<210> 12
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12
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Gly Arg Gly Leu Phe Gly Lys Gly Arg Asp Pro
 1               5                  10
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<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
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      Ogataea Minuta URA3 gene

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<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
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<212> DNA
<213> Ogataea minuta

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<210> 16
<211> 265
<212> PRT
<213> Ogataea minuta

<400> 16

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        35   40   45

Leu Asp Lys Leu Gly Pro Phe Ile Cys Leu Val Lys Thr His Ile Asp
    50   55   60

Ile Val Glu Asp Phe Ser Tyr Glu Asn Thr Val Val Pro Leu Leu Lys
65   70   75   80

Leu Ala Lys Lys His Asn Phe Met Ile Phe Glu Asp Arg Lys Phe Ala
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Ile Ala Lys Trp Ala Asp Ile Thr Asn Ala His Gly Val Thr Gly Ser
        115   120   125

Arg Ile Val Ser Gly Leu Arg Gln Ala Ala Gln Glu Thr Thr Asp Glu
    130   135   140

Pro Arg Gly Leu Leu Met Leu Ala Glu Leu Ser Ser Glu Gly Ser Leu
145   150   155   160

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            165   170   175

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        180   185   190

Asp Glu Gly Phe Asp Trp Leu Ile Met Thr Pro Gly Val Gly Leu Asp
        195   200   205

Asp Thr Gly Asp Ala Leu Gly Gln Gln Tyr Arg Thr Val Ser Ala Val
    210   215   220

Met Lys Thr Gly Thr Asp Ile Ile Ile Val Gly Arg Gly Leu Phe Gly
225   230   235   240

Lys Gly Arg Asp Pro Val Val Glu Gly Glu Arg Tyr Arg Lys Ala Gly
            245   250   255

Trp Asp Ala Tyr Leu Ser Arg Val Ala
            260   265

<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of a gene fragment
      conferring resistance against chloramphenicol

<400> 17
atggagaaaa aaactagtgg atataccacc   30

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of a gene fragment
      conferring resistance against chloramphenicol

<400> 18
ctgagacgaa aaagatatct caataaaccc                                    30


<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DU5 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 19
aggaagaaga ggaggaagag gaagaaac                                      28


<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DUC5 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 20
cgatgccatt gggatatatc aacggtgg                                      28


<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DU3 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 21
ccgtgtttga gtttgtgaaa aaccagggc                                     29


<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer DUC3 used for confirmation of destruction
      of Ogataea minuta URA3 gene

<400> 22
tgtggcgtgt tacggtgaaa acctggcc                                        28


<210> 23
<211> 14
<212> PRT
<213> Saccharomyces cerevisiae

<400> 23
Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met
  1               5                  10


<210> 24
<211> 14
<212> PRT
<213> Saccharomyces cerevisiae

<400> 24
Gln Asp Ser Tyr Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr
  1               5                  10


<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAD5 for amplification of 5'-region of
      Ogataea minuta ADE1 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (9)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t
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```
<220>
<221> modified_base
<222> (24)
<223> a, c, g or t

<220>
<221> modified_base
<222> (27)
<223> a, c, g or t

<220>
<221> modified_base
<222> (36)
<223> a, c, g or t

<400> 25
ttygtngcna cngaymgnat hwsngcntay gaygtnatha tg                    42


<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAD3 for amplification of 3'-region of
      Ogataea minuta ADE1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (33)
<223> a, c, g or t

<400> 26
gtnarccart cncknarraa ytgyttrtcr tanswrtcyt g                     41


<210> 27
<211> 2560
<212> DNA
<213> Ogataea minuta
```

<400> 27
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gatatcccaa gaacctatgc cgagggttca gctcacggcc gataaaccaa tcaaagacaa 60
cgtttcctga gtttcctcca acggccagga ttatctcgtg agttcccaga ccgttcggct 120
tgcgtgtggg cacgaacgag cccacgtaga caaacaggct caaagccaac gaaaactcgt 180
acgcagtcac catcaattcc agaaagttct cgtggatgaa cgacagctca ggaaggttga 240
actttgtgag ataagctctg ctggcaagaa ttcccacgag aagagtgctc aattctttcc 300
cgttgacgag atagttgagc tttgttccgt ctcgtaacag gactccctct ttatggtagc 360
caggcatcac aagatccacc aacgtcagag tgaagaacca caccaggtaa accttccagc 420
acgtgacatt taacacaaga tcccgccagt tgccgactat cttggactcg aaaagcgttt 480
tcagcgtggc aaaatcgatg cttgcgcctt caaccacata ctcctcatta cagcaaaagt 540
agaggaaaag gaccactgaa gggagaaata ctgacaaaac gaccgctccc ggtgtcccgc 600
agaaatcttt atgcgtagtc ttggggttca attcagacat ggtagattgg tgagggtaat 660
tgtgaagagg attcgataaa gagagggaa cagcaccgga gatagttctt agatcaaaat 720
gtttttctga cctttttgc tctttctcgt ttagctcgcg tacagtcgac gcgtcggttt 780
gcgtcgaaaa gagtcaagcc gcgatcgcga ttaaaaatga atccggagaa gtcaaaaata 840
tgtaatttaa accatcacag tatataagta ggcgggaagc gcacaatttc taggcattcc 900
acagatcagc taaccaggac attccactgg agccaacaat gtcactcaca acaaccaacc 960
tcgacggcat cttgccgcta attgccaagg gcaaagtcag agacatctat caagttgacg 1020
aggaaagcct gctgttcgtg gcaacagacc ggattccgc ctacgatgtg atcatggaga 1080
atggaatcaa agacaagggt aaaatactga ctcagctgtc agtattctgg tttgatttgc 1140
tgaaagacac tatcaagaac caccttatcg catccactga cgacgaagtg tttgccagac 1200
ttccacagga gctgtctcag ccaaagtaca agtcgcagct gagtggaaga gcactggtgg 1260
tgagaaagca caaattgatc cccctggagg tgattgtcag aggctacatc accggaagtg 1320
catggaagga gtacaacaag agcaagaccg tgcacggtct cgaggttggc gcagagctga 1380
aggagagtca agagttcccc gttccgattt tcaccccgtc aacgaaagct gaacaaggcg 1440
aacacgacga aaacatttcc cccgagaaag ctgcagagat tgtcggggaa caactgtgtg 1500
cgcggctcgc agaaaaggct gtgcagctgt actccaaggc cagaacttac gccaaaagca 1560
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ttcttgtgga cgaggttttg acccctgatt cctcgagatt ttgggacgca aagacttaca 1680
agatcggaca gtcgcaggac tcttacgaca aacagtttct gagagactgg ctcacgtcca 1740
acggtctgaa cgggaaagac ggtgtctcta tgaccgcgga gatcgctgaa cgcacgggtg 1800
cgaagtacgt cgaggcattt gagtctctga cgggaagaaa gtggacgtag tttttgataa 1860
tagtaaccct ggaaatttga tatgtggcgg tgtagtctgt ggcggtggaa taaatctaa 1920
attgaattta gtcgcttccc aaaacagcaa tttgtcaaca cttagtctgt gcacagcctt 1980
gacggcattt gagccatccc agggtctggc agttacaggg ctttgatcaa aagaaaactg 2040
gtgaagtttg acaacaggct acagctgcca agtcgcaact tgggtagtag ctcattcgtc 2100
gaacaccagt gcgccatgtc catcgccaac gagttccagc ccttggagct tattggtagg 2160
ggttcctttg gatgtgttcg gaaagtgcgc cgcaagtcgg acggcaagat atttgtgaga 2220
aaggagatct cctacatcgc catgaacacc aaagagaagc agcagctcac agcagagttt 2280
cgtattctca gagaactaaa gcatcccaac attgtccatt atgtccacca cgaccacgtc 2340
caggaggaac agaccgtcca tctgtacatg gaatactgcg atggggggcga cttgtcggtg 2400
ttgatcagga agtacaaagg aaagaacgag tttatcccgg agaacttgat ctggcaaatc 2460
ttcacccagg ttctcaacgc tctctatcaa tgccactatg gggtcaatat tgaggctgtg 2520
caagaacttt tccagtccac tccagagatt gcaccccggg 2560
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<210> 28
<211> 303
<212> PRT
<213> Ogataea minuta

<400> 28
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Met Ser Leu Thr Thr Thr Asn Leu Asp Gly Ile Leu Pro Leu Ile Ala
 1               5                  10                  15


Lys Gly Lys Val Arg Asp Ile Tyr Gln Val Asp Glu Glu Ser Leu Leu
            20                  25                  30
```

```
Phe Val Ala Thr Asp Arg Ile Ser Ala Tyr Asp Val Ile Met Glu Asn
        35              40              45

Gly Ile Lys Asp Lys Gly Lys Ile Leu Thr Gln Leu Ser Val Phe Trp
    50              55              60

Phe Asp Leu Leu Lys Asp Thr Ile Lys Asn His Leu Ile Ala Ser Thr
65              70              75              80

Asp Asp Glu Val Phe Ala Arg Leu Pro Gln Glu Leu Ser Gln Pro Lys
            85          .       90              95

Tyr Lys Ser Gln Leu Ser Gly Arg Ala Leu Val Val Arg Lys His Lys
            100             105             110

Leu Ile Pro Leu Glu Val Ile Val Arg Gly Tyr Ile Thr Gly Ser Ala
        115             120             125

Trp Lys Glu Tyr Asn Lys Ser Lys Thr Val His Gly Leu Glu Val Gly
    130             135             140

Ala Glu Leu Lys Glu Ser Gln Glu Phe Pro Val Pro Ile Phe Thr Pro
145             150             155             160

Ser Thr Lys Ala Glu Gln Gly Glu His Asp Glu Asn Ile Ser Pro Glu
            165             170             175

Lys Ala Ala Glu Ile Val Gly Glu Gln Leu Cys Ala Arg Leu Ala Glu
            180             185             190

Lys Ala Val Gln Leu Tyr Ser Lys Ala Arg Thr Tyr Ala Lys Ser Lys
        195             200             205

Gly Ile Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asn
    210             215             220

Asp Glu Leu Val Leu Val Asp Glu Val Leu Thr Pro Asp Ser Ser Arg
225             230             235             240

Phe Trp Asp Ala Lys Thr Tyr Lys Ile Gly Gln Ser Gln Asp Ser Tyr
            245             250             255

Asp Lys Gln Phe Leu Arg Asp Trp Leu Thr Ser Asn Gly Leu Asn Gly
            260             265             270

Lys Asp Gly Val Ser Met Thr Ala Glu Ile Ala Glu Arg Thr Gly Ala
        275             280             285

Lys Tyr Val Glu Ala Phe Glu Ser Leu Thr Gly Arg Lys Trp Thr
    290             295             300


<210> 29
<211> 60
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      5'-primer for amplification of upstream region
      of URA3 structural gene

<400> 29
ccccgagctc aaaaaaaagg taccaatttc agctccgacg ccggagccca ctacgcctac 60


<210> 30
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      3'-primer for amplification of upstream region
      of URA3 structural gene

<400> 30
gggaagcttc cccagttgta caccaatctt gtcgacag                          38


<210> 31
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad1-5 used for destruction of Ogataea
      minuta ADE1 gene

<400> 31
aaaaagcggc cgctcccggt gtcccgcaga aatctttatg cgtagtcttg            50


<210> 32
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad1-3 used for destruction of Ogataea
      minuta ADE1 gene

<400> 32
cccccggatc cttttttttta agcttgttgt actccttcca tgcacttccg gtgatg    56


<210> 33
<211> 59
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad2-5 used for destruction of Ogataea
      minuta ADE1 gene

<400> 33
ttttcacccc gtcaaggatc cctgaacaag gcgaacacga cgaaaacatt tcccccgag   59

<210> 34
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer Dad2-3 used for destruction of Ogataea
      minuta ADE1 gene

<400> 34
tttttgggcc cacctgggtg aagatttgcc agatcaagtt ctcc   44

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DA5 used for confirmation of destruction
      of Ogataea minuta ADE1 gene

<400> 35
gatgcttgcg ccttcaacca catactcctc   30

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DA3 used for confirmation of destruction
      of Ogataea minuta ADE1 gene

<400> 36
aaaagttctt gcacagcctc aatattgacc   30

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DOU5 used for confirmation of destruction
      of Ogataea minuta ADE1 gene

<400> 37
atcgatttcg agtgtttgtc caggtccggg   30

<210> 38
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (3)
<223> His or Arg

<220>
<221> MOD_RES
<222> (4)
<223> Ile or Val

<400> 38
Pro Gln Xaa Xaa Trp Gln Thr Trp Lys Val
  1   5   10

<210> 39
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<400> 39
Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp
  1   5   10

<210> 40
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer POH5 for amplification of 5'-region of
      Ogataea minuta OCH1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

```
<400> 40
ccncarcryr thtggcarac ntggaargt                                    29


<210> 41
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer POH3 for amplification of 3'-region of
      Ogataea minuta OCH1 gene

<220>
<221> modified_base
<222> (19)
<223> a, c, g or t

<220>
<221> modified_base
<222> (22)
<223> a, c, g or t

<220>
<221> modified_base
<222> (25)
<223> a, c, g or t

<400> 41
ccaytgrcar aaytgdatnc knckngcrta cca                               33


<210> 42
<211> 2527
<212> DNA
<213> Ogataea minuta

<400> 42
agatctgttg acactggtca agcgtgtagc caagagaata ggaaacggaa tttcatactg 60
ccggcacaca aggacaataa gggcgtccgg ggctgtcgaa attgtcgaga ccgtagagct 120
attgttacct caataagttg ctctacgatt gtttccgtct ttgacaaagc agtaggcctt 180
tctcaaggtg gtgtacgggt gtttcatttt taatttgcat cgagaacgcg tagtgcgcca 240
atggatctgc aggggctcg gctgattgca ctgaaatttc agcaataaat agctgaggat 300
attcaggcac aacggtacca acggggcagg cttgatcgcg aagcagcagg agaaggcagc 360
gaagtgactg aagagacgag aaggagacga atcagcctac ccctggaacc ataaacaaag 420
tcgagccgtt tttttaggga cagaaaccgt tctggatatt tattcgacgc agagactcgg 480
tagtcatctc tacgttcagc acacaccatg aactatcacg acttgtacga tgatagcaaa 540
cggcagtcgt tgatgcgaaa ggcgcgaaag ttcgctgaga tgaacaagaa gttggtggtg 600
gtggtcattt taacgatgta cgttgtgtcg cgtctggcgt cggttggaag cacgaaacag 660
gagtcgattc caggactcac catgaaagag tcagagttag aggtgaattt taaaacattt 720
ggaatggatc tgcagaagcg gaacgagcta ccggccgcaa gtgcaacgct gagagaaaaa 780
ctatcgtttt acttcccta tgaccctgaa aaaccagtgc ccaaccaaat atggcagacg 840
tggaaagtgg acatcaacga caaatcattc ccgagacact tccgtaagtt ccaagagaca 900
tggccacaac taaacagcgg gtacacgtac catctcattc cagacagtat tgtggacgag 960
ttcatgagga gtcttttgc caatgtccct gaggttattg cagcctacaa catgttaccg 1020
aaaaatatcc tcaaggcgga ttttttccgg tatttggtga tttttgcgcg cggtggaact 1080
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tattcggata tcgacacgat ctgcctcaaa ccagtgaacg aatgggccac gtttaacgaa 1140
caaactgtca tttcgcacta tctcaagacc aacggtaaaa cctcgcagtt gccagaagtg 1200
gacccctcca cgcgcaaaac accgatcgga ctcaccattg gaatagaggc cgacccagac 1260
agacccgact ggcacgaatg gtacgctaga cgtattcagt tctgtcaatg gacgatccag 1320
ggcaagcaag gccatcccat gctgcgcgag ttgatcatcc gtatagtgga gcaaactttc 1380
cgcaaagagg ccatgggcaa tttgaaaaaa gtagagggga aggatatggg tggtgacatc 1440
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gtgagtgacg gaaagctggg agacggttac ggagtcgggt ccaagtactg gaacagtcac 1560
gccaagtaca agctgtctca cattgaggtg gatgccaaca acgagccgat gcactctgac 1620
aagcaaacta tcagctggaa gtccatgagt aagctatcgg agccctgat tatagatgac 1680
gtgatgatcc tgccaatcac tagcttcagc cccggcgtgg gccagatggg ctcgcattcg 1740
cccgaccacc cgctcgcatt tgtccggcac atgttccagg gcagctggaa accagatgca 1800
gagaagatgt gactgcatat aggaacgcat tttatacagt agatcaagtt aaaagtttga 1860
acttttgcgg ggaagtggtg taagggtgtt tgacgagggc ctgaacccgt gagtcaacgc 1920
gcttggacgg aagaacgggt gcacgccgca tggggctgtt cgttcagttt tgacgctgct 1980
aacgagagag tagcttgcag attgcaatcc cgactgagtc cacccggttg agctagtcac 2040
acgactgcgt cttttctttc tggtgtacgg gtgtcaatac attttcggtt taaaaacgat 2100
aagatgcaac aaggtatctt ctgtagctaa accccacttc tccagacacc ttccaccagc 2160
cgatgactat gacagacagg tttttggagg attacaagaa gtttctcccc aaagcgcacg 2220
atttgagggg cacgcactca cggctttttca cgacggcggg cggggccgat gcggggagtt 2280
tggctgattg gagagagtgg acagatgatt tgggtcattc gcaggagtat tacgagctga 2340
aacaggagat caattgtctt gttcttaact accttatcta cgaaggatat gttggtgctg 2400
ttcgagagtt ttcgaaagag ctgggattcg attttatcgt ggaggagttg gaaggaattg 2460
aagaggagaa gggaggccac caagaggacg gagagtacac gaccatgtca gacactgacg 2520
tactagt                                                          2527
```

<210> 43
<211> 434
<212> PRT
<213> Ogataea minuta

<400> 43

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Met Asn Tyr His Asp Leu Tyr Asp Asp Ser Lys Arg Gln Ser Leu Met
 1               5                  10                  15

Arg Lys Ala Arg Lys Phe Ala Glu Met Asn Lys Lys Leu Val Val Val
            20                  25                  30

Val Ile Leu Thr Met Tyr Val Val Ser Arg Leu Ala Ser Val Gly Ser
        35                  40                  45

Thr Lys Gln Glu Ser Ile Pro Gly Leu Thr Met Lys Glu Ser Glu Leu
    50                  55                  60

Glu Val Asn Phe Lys Thr Phe Gly Met Asp Leu Gln Lys Arg Asn Glu
65                  70                  75                  80

Leu Pro Ala Ala Ser Ala Thr Leu Arg Glu Lys Leu Ser Phe Tyr Phe
                85                  90                  95

Pro Tyr Asp Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr Trp
            100                 105                 110

Lys Val Asp Ile Asn Asp Lys Ser Phe Pro Arg His Phe Arg Lys Phe
        115                 120                 125
```

Gln Glu Thr Trp Pro Gln Leu Asn Ser Gly Tyr Thr Tyr His Leu Ile
    130   135   140

Pro Asp Ser Ile Val Asp Glu Phe Met Arg Ser Leu Phe Ala Asn Val
145   150   155   160

Pro Glu Val Ile Ala Ala Tyr Asn Met Leu Pro Lys Asn Ile Leu Lys
            165   170   175

Ala Asp Phe Phe Arg Tyr Leu Val Ile Phe Ala Arg Gly Gly Thr Tyr
            180   185   190

Ser Asp Ile Asp Thr Ile Cys Leu Lys Pro Val Asn Glu Trp Ala Thr
            195   200   205

Phe Asn Glu Gln Thr Val Ile Ser His Tyr Leu Lys Thr Asn Gly Lys
    210   215   220

Thr Ser Gln Leu Pro Glu Val Asp Pro Ser Thr Arg Lys Thr Pro Ile
225   230   235   240

Gly Leu Thr Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His
            245   250   255

Glu Trp Tyr Ala Arg Arg Ile Gln Phe Cys Gln Trp Thr Ile Gln Gly
            260   265   270

Lys Gln Gly His Pro Met Leu Arg Glu Leu Ile Ile Arg Ile Val Glu
            275   280   285

Gln Thr Phe Arg Lys Glu Ala Met Gly Asn Leu Lys Lys Val Glu Gly
    290   295   300

Lys Asp Met Gly Gly Asp Ile Met Gln Trp Thr Gly Pro Gly Val Phe
305   310   315   320

Thr Asp Thr Leu Phe Asp Tyr Leu Asn Asn Val Val Ser Asp Gly Lys
            325   330   335

Leu Gly Asp Gly Tyr Gly Val Gly Ser Lys Tyr Trp Asn Ser His Ala
            340   345   350

Lys Tyr Lys Leu Ser His Ile Glu Val Asp Ala Asn Asn Glu Pro Met
    355   360   365

His Ser Asp Lys Gln Thr Ile Ser Trp Lys Ser Met Ser Lys Leu Ser
    370   375   380

Glu Pro Leu Ile Ile Asp Asp Val Met Ile Leu Pro Ile Thr Ser Phe
385   390   395   400

Ser Pro Gly Val Gly Gln Met Gly Ser His Ser Pro Asp His Pro Leu
            405   410   415

Ala Phe Val Arg His Met Phe Gln Gly Ser Trp Lys Pro Asp Ala Glu
            420   425   430

Lys Met

```
<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DO3 used for confirmation of destruction
      of Ogataea minuta OCH1 gene

<400> 44
ccattgtcag ctccaattct ttgataaacg                                    30


<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DO5 used for confirmation of destruction
      of Ogataea minuta OCH1 gene

<400> 45
acacttccgt aagttccaag agacatggcc                                    30


<210> 46
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DO3-2 used for confirmation of destruction
      of Ogataea minuta OCH1 gene

<400> 46
tcaccacgtt attgagataa tcaaacaggg                                    30


<210> 47
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

<400> 47
Thr Asn Tyr Leu Asn Ala Gln Tyr
  1                   5
```

```
<210> 48
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

<400> 48
Lys Ala Tyr Trp Glu Val Lys Phe
 1               5


<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPA5 for amplification of 5'-region of
      Ogataea minuta PEP4 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<400> 49
acnaaytayy tnaaygcnca rta                                      23


<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPA3 for amplification of 3'-region of
      Ogataea minuta PEP4 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t
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<400> 50
aayttnacyt cccartangc ytt   23

<210> 51
<211> 1951
<212> DNA
<213> Ogataea minuta

<220>
<221> modified_base
<222> (35)
<223> a, c, g or t

<400> 51
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gctaatcacg aagatttttg gatttcctga tctgtagtgt atccatcctg ccttaatcgt 180
tttcgataca tttgttatcc gaattgggaa tggcattagt cgtgcgccac ccgactcgcc 240
accccattc tagtggcaaa caggattgaa agagggctaa aaggtaactt agtgtttat 300
ctctgaatct tccttctgat atcaatcaac aattgttaaa cgattgaaag ttttgaaaca 360
ttcattgaac ttgcgaagcg ctcacacagc atcgttcggt tagcagttac aacagtttag 420
gtttttttcc ccacaaaaag gctcacgctg cctcctcact cttgcctctt ttcttgatga 480
aactctcgct tgcattgctc gcccttggtg gtttccaaga ggcccacgcc aaggttcatc 540
atgcgccaat caagaagact cctgccgcgg aaacttacaa ggacgtgagt ttcggcgact 600
acgtggattc tctgaagggc aagtatgtct ctatgtttgc taagcatgct gcggagtcct 660
cccaaaacgc ctttgtccct tttgttcagg aagtgcaaga cccagagttt actgttcagg 720
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tggtatgttt attgctttta ttacgtgacc aaatgttggt ttttctttca ccttttactc 1860
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tgaattgcac aaatttaaag attgctctag a   1951

<210> 52
<211> 410
<212> PRT
<213> Ogataea minuta

<400> 52

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Met Lys Leu Ser Leu Ala Leu Leu Ala Leu Gly Gly Phe Gln Glu Ala
 1           5                   10                  15

His Ala Lys Val His His Ala Pro Ile Lys Lys Thr Pro Ala Ala Glu
            20              25                  30

Thr Tyr Lys Asp Val Ser Phe Gly Asp Tyr Val Asp Ser Leu Lys Gly
        35                  40                  45

Lys Tyr Val Ser Met Phe Ala Lys His Ala Ala Glu Ser Ser Gln Asn
    50                  55                  60

Ala Phe Val Pro Phe Val Gln Glu Val Gln Asp Pro Glu Phe Thr Val
65                  70                  75                  80

Gln Glu Gly His Asn Ser Pro Leu Thr Asn Tyr Val Asn Ala Gln Tyr
            85                  90                  95

Phe Thr Glu Ile Gln Ile Gly Thr Pro Gly Gln Pro Phe Lys Val Ile
            100                 105                 110

Leu Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Gly Ser Asp Cys Ser
        115                 120                 125

Ser Leu Ala Cys Tyr Leu His Gln Lys Tyr Asp His Asp Ser Ser Ser
    130                 135                 140

Thr Tyr Lys Ala Asn Gly Ser Glu Phe Ala Ile Arg Tyr Gly Ser Gly
145                 150                 155                 160

Ser Leu Glu Gly Phe Val Ser Gln Asp Thr Leu Thr Leu Gly Asp Leu
            165                 170                 175

Ile Ile Pro Lys Gln Asp Phe Ala Glu Ala Thr Ser Glu Pro Gly Leu
            180                 185                 190

Ala Phe Ala Phe Gly Lys Phe Asp Gly Ile Leu Gly Leu Ala Tyr Asp
        195                 200                 205

Thr Ile Ser Val Asp Lys Ile Val Pro Pro Ile Tyr Asn Ala Leu Asn
    210                 215                 220

Leu Gly Leu Leu Asp Glu Pro Gln Phe Ala Phe Tyr Leu Gly Asp Thr
225                 230                 235                 240

Ala Lys Ser Glu Ala Asp Gly Gly Val Ala Thr Phe Gly Gly Val Asp
            245                 250                 255

Glu Thr Lys Tyr Asp Gly Lys Ile Thr Trp Leu Pro Val Arg Arg Lys
            260                 265                 270

Ala Tyr Trp Glu Val Lys Phe Asp Gly Ile Ala Leu Gly Asp Glu Tyr
        275                 280                 285

Ala Thr Leu Asp Gly Tyr Gly Ala Ala Ile Asp Thr Gly Thr Ser Leu
        290                 295                 300
```

```
Ile Ala Leu Pro Ser Gln Leu Ala Glu Ile Leu Asn Ser Gln Ile Gly
305             310             315             320

Ala Glu Lys Ser Trp Ser Gly Gln Tyr Thr Ile Asp Cys Glu Lys Arg
            325             330             335

Ala Ser Leu Pro Asp Leu Thr Phe Asn Phe Asp Gly Tyr Asn Phe Ser
            340             345             350

Ile Ser Ala Tyr Asp Tyr Thr Leu Glu Val Ser Gly Ser Cys Ile Ser
        355             360             365

Ala Phe Thr Pro Met Asp Phe Pro Ala Pro Ile Gly Pro Leu Ala Ile
    370             375             380

Ile Gly Asp Ala Phe Leu Arg Lys Tyr Tyr Ser Val Tyr Asp Leu Gly
385             390             395             400

Lys Asp Ala Val Gly Leu Ala Lys Ala Val
            405             410
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<210> 53
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (2)
<223> Gly or Leu

<400> 53
Asp Xaa Asn Gly His Gly Thr His Cys Ala Gly
 1               5                  10


<210> 54
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (6)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (9)
<223> Val or Ile

<220>
<221> MOD_RES
<222> (10)
<223> Ala or Val
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<400> 54
Gly Thr Ser Met Ala Xaa Pro His Xaa Xaa Gly
  1               5                   10
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```
<210> 55
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPB5 for amplification of 5'-region of
      Ogataea minuta PRB1 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

<220>
<221> modified_base
<222> (30)
<223> a, c, g or t

<400> 55
gaybknaayg gncayggnac ncaytgykcn gg                              32
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<210> 56
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PPB3 for amplification of 3'-region of
      Ogataea minuta PRB1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t
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<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<220>
<221> modified_base
<222> (24)
<223> a, c, g or t

<220>
<221> modified_base
<222> (27)
<223> a, c, g or t

<220>
<221> modified_base
<222> (30)
<223> a, c, g or t

<400> 56
ccnrcnayrt gnggnwsngc catnwsngtn cc                                      32


<210> 57
<211> 2214
<212> DNA
<213> Ogataea minuta

<400> 57
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cagatcccaa atttgccacc agactaaatt ggggcattct ggtgagggaa taggggaaat 180
aagagggtgt tttgacgttt catatacatt gctctttctt ttcttggacg gttagcggta 240
ttgccataga ttatcttgcg cagttcagca tccttaggag ttattctttc ttgtaggtct 300
tttttcagaa cagaaaaatc gccaatcaca gaaagattca gtcctaattg aagccttatc 360
ttatcttatc tcacctcaac cacttgaacc aaaatgaagt tatcccagtc tgctgcggtg 420
gctattctgt cttcgttggc agcagtggag gccttggtca tcccgttatt tgacgacttg 480
ccagcagagt ttgcccttgt tccaatggat gcgaaagcgg aagtcatttc tgacgttcct 540
gtcgactcgg ccattagtga tgctcctatc gcggcactaa atgatgctcc aagccctctc 600
gtcacatcgc tgatcgcatc tcaaaatttg attccaaact cttatattgt cgttttcaag 660
aatggcctag cttccggggc agttgacttc cacatggagt ggctcaagga aacgcactcc 720
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caaaccctgg ctgctttgtc taaggacatg ccagcagaag aattggccgc cgaaggtttc 780
gtttccgaaa gcattgatct tactgaggtg tttagcatct ccgatttgtt cagtggatat 840
accggatact ccccggagaa ggtggttgac ctcatcagaa gacaccctga cgtggcgttc 900
gttgagcagg actcgagagt tttcgccgat aagtcgtcta ctcaaaacgg tgctccttgg 960
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cgcttttcct tttttttctg ttgtttggag tgtttgtttt tctggataat gtggttagtt 2160
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<210> 58
<211> 539
<212> PRT
<213> Ogataea minuta

<400> 58

Met	Lys	Leu	Ser	Gln	Ser	Ala	Ala	Val	Ala	Ile	Leu	Ser	Ser	Leu	Ala
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Ala	Val	Glu	Ala	Leu	Val	Ile	Pro	Leu	Phe	Asp	Asp	Leu	Pro	Ala	Glu
			20				25					30			

Phe	Ala	Leu	Val	Pro	Met	Asp	Ala	Lys	Ala	Glu	Val	Ile	Ser	Asp	Val
		35				40					45				

Pro	Val	Asp	Ser	Ala	Ile	Ser	Asp	Ala	Pro	Ile	Ala	Ala	Leu	Asn	Asp
	50					55					60				

Ala	Pro	Ser	Pro	Leu	Val	Thr	Ser	Leu	Ile	Ala	Ser	Gln	Asn	Leu	Ile
65					70				75						80

Pro	Asn	Ser	Tyr	Ile	Val	Val	Phe	Lys	Asn	Gly	Leu	Ala	Ser	Gly	Ala
				85					90					95	

Val	Asp	Phe	His	Met	Glu	Trp	Leu	Lys	Glu	Thr	His	Ser	Gln	Thr	Leu
			100					105					110		

Ala	Ala	Leu	Ser	Lys	Asp	Met	Pro	Ala	Glu	Glu	Leu	Ala	Ala	Glu	Gly
		115					120					125			

Phe Val Ser Glu Ser Ile Asp Leu Thr Glu Val Phe Ser Ile Ser Asp
    130   135   140

Leu Phe Ser Gly Tyr Thr Gly Tyr Phe Pro Glu Lys Val Val Asp Leu
145   150   155   160

Ile Arg Arg His Pro Asp Val Ala Phe Val Glu Gln Asp Ser Arg Val
            165   170   175

Phe Ala Asp Lys Ser Ser Thr Gln Asn Gly Ala Pro Trp Gly Leu Ser
            180   185   190

Arg Ile Ser His Arg Glu Pro Leu Ser Leu Gly Asn Phe Asn Glu Tyr
        195   200   205

Val Tyr Asp Asp Leu Ala Gly Asp Gly Val Thr Ala Tyr Val Ile Asp
    210   215   220

Thr Gly Ile Asn Val Lys His Glu Gln Phe Gly Gly Arg Ala Glu Trp
225   230   235   240

Gly Lys Thr Ile Pro Thr Gly Asp Asp Asp Ile Asp Gly Asn Gly His
            245   250   255

Gly Thr His Cys Ala Gly Thr Ile Gly Ser Glu Asp Tyr Gly Val Ser
            260   265   270

Lys Asn Ser Lys Ile Val Ala Val Lys Val Leu Arg Ser Asn Gly Ser
        275   280   285

Gly Ser Met Ser Asp Val Ile Lys Gly Val Glu Phe Ala Ala Asn Asp
    290   295   300

His Val Ala Lys Ser Lys Ala Lys Lys Asp Gly Phe Lys Gly Ser Thr
305   310   315   320

Ala Asn Met Ser Leu Gly Gly Gly Lys Ser Pro Ala Leu Asp Leu Ala
            325   330   335

Val Asn Ala Ala Val Lys Ala Gly Leu His Phe Ala Val Ala Ala Gly
            340   345   350

Asn Asp Asn Ala Asp Ala Cys Asn Tyr Ser Pro Ala Ala Ala Glu Asn
        355   360   365

Ala Val Thr Val Gly Ala Ser Thr Leu Ser Asp Ser Arg Ala Tyr Phe
    370   375   380

Ser Asn Tyr Gly Lys Cys Val Asp Ile Phe Ala Pro Gly Leu Asn Ile
385   390   395   400

Leu Ser Thr Tyr Ile Gly Ser Asp Thr Ala Thr Ala Thr Leu Ser Gly
            405   410   415

Thr Ser Met Ala Ser Pro His Val Cys Gly Leu Leu Thr Tyr Phe Leu
            420   425   430

Ser Leu Gln Pro Glu Ser Ser Ser Leu Phe Ser Ser Ala Ala Ile Ser
     435   440   445

Pro Ala Gln Leu Lys Lys Asn Leu Ile Lys Phe Gly Thr Lys Asn Val
     450   455   460

Leu Ser Glu Ile Pro Ser Asp Gly Thr Pro Asn Ile Leu Ile Tyr Asn
465   470   475   480

Gly Ala Gly Lys Asn Ile Ser Asp Phe Trp Ala Phe Glu Asp Glu Ala
          485   490   495

Ser Ala Lys Ser Asp Leu Lys Lys Ala Val Asp Ile Ala Thr Ser Val
          500   505   510

Asp Leu Asp Leu Gln Asp Ile Lys Glu Lys Phe Asn His Ile Leu Glu
          515   520   525

Glu Val Ala Glu Glu Val Ala Asp Leu Phe Asp
     530   535

<210> 59
<211> 9
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<221> MOD_RES
<222> (1)
<223> His or Asn

<220>
<221> MOD_RES
<222> (5)
<223> Val or Thr

<400> 59
Xaa Tyr Asp Trp Xaa Phe Leu Asn Asp
  1   5

<210> 60
<211> 12
<212> PRT
<213> Saccharomyces cerevisiae

<400> 60
Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Glu Ile
  1   5   10

<210> 61
<211> 26
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      primer PKR5 for amplification of 5'-region of
      Ogataea minuta KTR1 gene

<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

<400> 61
maytaygayt ggrynttyyt naayga                                          26


<210> 62
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PKR3 for amplification of 3'-region of
      Ogataea minuta KTR1 gene

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (27)
<223> a, c, g or t

<400> 62
atytcraart tnswccaraa rtgrcanarr ttrta                                35


<210> 63
<211> 1930
<212> DNA
<213> Ogataea minuta

<400> 63
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acaatggcta gagcgaatgc gaggctgatc cggtttgcaa tctttgctac cgtgttggtt 180
ttatgtggat acattttatc caagggctcg tctacttcgt atacgatttc gacgccagag 240
tccggctcga gttccagtgg cactgttgct aatactgaga aatctgccct cgcagtgggt 300
gagaaaagcg ttgcaggcgc agccgagaaa agcgttcctg cagctgacgt cccagatgga 360
aaggtgaagg ccacttttgt ctctttggcc agaaaccagg atctgtggga gctggtgaac 420
tcgatcagac aggtcgaaga ccgttcaac aacaagtatc attacgattg ggtgttcttg 480
aacgacgcgg aattcaacga cgagttcaag aaggtgacct ctcaggtctg ttcgggtaag 540
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aaggctgctg ccaccagaga gcaaatgaga aaggacaaga tcatctacgg agactccatc 660
tcgtacagac acatgtgcag atacgagtcg ggattcttct tcaaacaccc agaactcgca 720
gagtacgagt actactggag agtggagcca agcatcaaga tctactgtga cattgactac 780
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<210> 64
<211> 403
<212> PRT
<213> Ogataea minuta

<400> 64

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Met Ala Arg Ala Asn Ala Arg Leu Ile Arg Phe Ala Ile Phe Ala Thr
 1               5                   10                  15

Val Leu Val Leu Cys Gly Tyr Ile Leu Ser Lys Gly Ser Ser Thr Ser
            20                  25                  30

Tyr Thr Ile Ser Thr Pro Glu Ser Gly Ser Ser Ser Ser Gly Thr Val
        35                  40                  45

Ala Asn Thr Glu Lys Ser Ala Leu Ala Val Gly Glu Lys Ser Val Ala
    50                  55                  60

Gly Ala Ala Glu Lys Ser Val Pro Ala Ala Asp Val Pro Asp Gly Lys
65                  70                  75                  80

Val Lys Ala Thr Phe Val Ser Leu Ala Arg Asn Gln Asp Leu Trp Glu
                85                  90                  95

Leu Val Asn Ser Ile Arg Gln Val Glu Asp Arg Phe Asn Asn Lys Tyr
            100                 105                 110

His Tyr Asp Trp Val Phe Leu Asn Asp Ala Glu Phe Asn Asp Glu Phe
        115                 120                 125

Lys Lys Val Thr Ser Gln Val Cys Ser Gly Lys Thr Lys Tyr Gly Val
    130                 135                 140
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Ile Pro Lys Glu Gln Trp Ser Phe Pro Ser Trp Ile Asp Thr Asp Lys
145   150   155   160

Ala Ala Ala Thr Arg Glu Gln Met Arg Lys Asp Lys Ile Ile Tyr Gly
                165   170   175

Asp Ser Ile Ser Tyr Arg His Met Cys Arg Tyr Glu Ser Gly Phe Phe
                180   185   190

Phe Lys His Pro Glu Leu Ala Glu Tyr Glu Tyr Tyr Trp Arg Val Glu
                195   200   205

Pro Ser Ile Lys Ile Tyr Cys Asp Ile Asp Tyr Asp Ile Phe Lys Phe
                210   215   220

Met Lys Asp Asn Lys Lys Ser Tyr Gly Trp Thr Ile Ser Leu Pro Glu
225   230   235   240

Tyr Lys Glu Thr Ile Pro Thr Leu Trp Lys Thr Thr Arg Asp Phe Met
                245   250   255

Lys Glu Asn Pro Gln Tyr Val Ala Gln Asp Asn Leu Ile Asn Phe Ile
                260   265   270

Ser Asp Asp Gly Gly Ser Ser Tyr Asn Gly Cys His Phe Trp Ser Asn
                275   280   285

Phe Glu Val Gly Ser Leu Glu Phe Trp Arg Gly Glu Ala Tyr Thr Lys
                290   295   300

Tyr Phe Glu Ala Leu Asp Gln Ala Gly Gly Phe Phe Tyr Glu Arg Trp
305   310   315   320

Gly Asp Ala Pro Ile His Ser Ile Ala Val Ala Leu Phe Met Pro Lys
                325   330   335

Asp Glu Val His Phe Phe Asp Asp Val Gly Tyr Phe His Asn Pro Phe
                340   345   350

His Asn Cys Pro Ile Asp Asn Ala Val Arg Glu Ala Lys Asn Cys Val
                355   360   365

Cys Asn Gln Ala Asp Asp Phe Thr Phe Gln His Tyr Ser Cys Thr Pro
                370   375   380

Lys Phe Tyr Gln Glu Met Gly Leu Lys Lys Pro Ala Asn Trp Glu Gln
385   390   395   400

Tyr Ile His

<210> 65
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae

<400> 65
Thr Ser Trp Val Leu Trp Leu Asp Ala Asp
 1   5   10

<210> 66
<211> 10
<212> PRT
<213> Saccharomyces cerevisiae

<400> 66
Glu Thr Glu Gly Phe Ala Lys Met Ala Lys
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<210> 67
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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      primer PMN5 for amplification of 5'-region of
      Ogataea minuta MNN9 gene

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<223> a, c, g or t

<220>
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<222> (6)
<223> a, c, g or t

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<222> (12)
<223> a, c, g or t

<220>
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<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (21)
<223> a, c, g or t

<220>
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<222> (27)
<223> a, c, g or t

<400> 67
acnwsntggg tnytntggyt ngaygcnga   29

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<210> 68
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PMN3 for amplification of 3'-region of
      Ogataea minuta MNN9 gene

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<222> (3)
<223> a, c, g or t

<220>
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<222> (12)
<223> a, c, g or t

<220>
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<222> (18)
<223> a, c, g or t

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<222> (24)
<223> a, c, g or t

<400> 68
ttngccatyt tngcraancc ytcngtytc                                              29


<210> 69
<211> 2221
<212> DNA
<213> Ogataea minuta

<400> 69
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t                                                                2221
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<210> 70
<211> 367
<212> PRT
<213> Ogataea minuta

<400> 70

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Met Leu Lys Gly Val Leu Lys His Pro Leu Val His Gln Ile Arg Arg
  1               5                  10                  15

Lys Pro Val Lys Val Leu Val Pro Val Phe Gly Leu Ala Val Leu Leu
              20                  25                  30

Phe Leu Val Phe Gly Gly Ser Ser Ser Asn Arg Lys Thr Asn Ser Pro
          35                  40                  45

Tyr Ser Tyr Lys Arg Asn Asn Arg Asp Glu Val Ile Pro Arg Asn Leu
      50                  55                  60

Pro Ala Asp His Ile Ser His Tyr Asp Leu Asn Asn Leu Ala Ser Thr
 65                  70                  75                  80

Pro Met Ala Ala Tyr Asn Lys Glu Arg Val Leu Ile Leu Thr Pro Met
              85                  90                  95

Ala Lys Phe Leu Asp Gly Tyr Trp Asp Asn Leu Leu Lys Leu Thr Tyr
             100                 105                 110

Pro Arg Asp Leu Ile Glu Leu Gly Phe Ile Val Pro Arg Thr Ala Glu
         115                 120                 125

Gly Asp Gln Ala Leu Lys Lys Leu Glu His Ala Val Lys Ile Ile Gln
     130                 135                 140

Asn Pro Lys Asn Thr Lys Glu Pro Lys Phe Ala Lys Val Thr Ile Leu
145                 150                 155                 160
```

```
Arg Gln Asp Asn Glu Ser Leu Ser Ser Gln Ser Glu Lys Asp Arg His
            165             170             175

Ala Phe Lys Val Gln Lys Glu Arg Arg Ala Gln Met Ala Thr Ala Arg
            180             185             190

Asn Ser Leu Leu Phe Thr Thr Ile Gly Pro Tyr Thr Ser Trp Val Leu
            195             200             205

Trp Leu Asp Ser Asp Ile Val Glu Ser Pro His Thr Leu Ile Gln Asp
    210             215             220

Leu Val Ser His Asp Lys Pro Val Ile Ala Ala Asn Cys Tyr Gln Arg
225             230             235             240

Tyr Tyr Asp Glu Asp Lys Lys Glu Asp Ser Ile Arg Pro Tyr Asp Phe
            245             250             255

Asn Asn Trp Ile Glu Ser Glu Glu Gly Leu Arg Ile Ala Ser Thr Met
            260             265             270

Ser Asp Asp Glu Ile Ile Val Glu Ala Tyr Ala Glu Ile Ala Thr Tyr
            275             280             285

Arg Pro Leu Met Gly His Phe Tyr Asp Pro Asn Gly Asp Leu Gly Thr
    290             295             300

Glu Met Gln Leu Asp Gly Val Gly Gly Thr Cys Leu Met Val Lys Ala
305             310             315             320

Asp Val His Arg Asp Gly Ala Met Phe Pro Asn Phe Pro Phe Tyr His
            325             330             335

Leu Ile Glu Thr Glu Gly Phe Ala Lys Met Ala Lys Arg Leu Gly Tyr
            340             345             350

Gln Val Phe Gly Leu Pro Asn Tyr Leu Val Phe His Tyr Asn Glu
            355             360             365
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<210> 71
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DMN5

<400> 71
agatgaggtg attccacgta atttgccagc   30

<210> 72
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer DMN3

<400> 72
ttttgattgt catctatttc gcacaccctg   30

<210> 73
<211> 12
<212> PRT
<213> Pichia pastoris

<400> 73
Gly Gly Gly Ser Ser Ile Asn Phe Met Met Tyr Thr
  1   5   10

<210> 74
<211> 10
<212> PRT
<213> Pichia pastoris

<400> 74
Asp Met Trp Pro Met Val Trp Ala Tyr Lys
  1   5   10

<210> 75
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAX5 for amplification of 5'-region of
      Ogataea minuta AOX1 gene

<220>
<221> modified_base
<222> (3)
<223> a, c, g or t

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (9)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

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<220>
<221> modified_base
<222> (15)
<223> a, c, g or t

<400> 75
ggnggnggnw snwsnathaa yttyatgatg tayac                              35


<210> 76
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer PAX3 for amplification of 3'-region of
      Ogataea minuta AOX1 gene

<220>
<221> modified_base
<222> (6)
<223> a, c, g or t

<220>
<221> modified_base
<222> (12)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<400> 76
ttrtangccc anaccatngg ccacatrtc                                     29


<210> 77
<211> 5817
<212> DNA
<213> Ogataea minuta

<400> 77
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aggcgcactt taaaagataa tctacatcca gaaaaataaa aaaataaaac tgaaccggca 120
tttgcgatta cgtaagccac aaaatttcag gaaactcgta caagatcagg ttggcgaggg 180
ggctagcgat agaatgtatc agtgttatta gtggctctag gagtagaaaa caatagaata 240
aagatccgaa gaaagggagc aagaaggcca cgccagacgt tctagtaggt agcccaatcg 300
tcaatgtagc tgttcaggtc tttcaacagg ttcttggtct cgtctggact ggagatccaa 360
caagtcgttg ctgcggttcg actggcatag tcgttggcgc cgagggagct gaactggtcg 420
ccgacgtgca gggtgttttc gggcttgatg gttcggttgt cgttgcagct gaggaactct 480
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cgcagaacca cctcttccag ctgctcgcga acgagtttgt agccttcttt ggggaccagt 660
ccaacggcac gctcctttct gatgatgatg gcatgcaatg aaagtttctt gatcaggtcc 720
gagaagatct cctgcgcaaa gtccagggtc cggatgatgt cttcctcgga ccagtcgagc 780
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```

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<210> 78
<211> 663
<212> PRT
<213> Ogataea minuta

<400> 78
Met Ala Ile Pro Asp Glu Phe Asp Ile Ile Val Val Gly Gly Gly Ser
  1               5                  10                      15

Cys Gly Cys Ala Ile Ala Gly Arg Leu Gly Asn Leu Asp Pro Asp Val
              20                  25                  30

Thr Val Ala Leu Ile Glu Gly Gly Glu Asn Asn Ile Asn Asn Pro Trp
          35                  40                  45

Val Tyr Leu Pro Gly Val Tyr Pro Arg Asn Met Arg Leu Asp Ser Lys
      50                  55                  60

Thr Ala Thr Phe Tyr Asn Ser Arg Pro Ser Lys His Leu Asn Gly Arg
 65                  70                  75                      80

Arg Ala Ile Val Pro Cys Ala Asn Ile Leu Gly Gly Gly Ser Ser Ile
              85                  90                      95

Asn Phe Leu Met Tyr Thr Arg Ala Ser Ala Ser Asp Tyr Asp Asp Trp
             100                 105                 110

Glu Gln Glu Gly Trp Thr Thr Asp Glu Leu Leu Pro Leu Met Lys Lys
         115                 120                 125
```

```
Leu Glu Thr Tyr Gln Arg Pro Cys Asn Asn Arg Glu Val His Gly Phe
    130             135             140

Asp Gly Pro Ile Lys Val Ser Phe Gly Asn Tyr Thr Tyr Pro Thr Ala
145             150             155             160

Gln Asp Phe Leu Arg Ala Cys Glu Ser Gln Gly Ile Pro Phe Asn Asp
            165             170             175

Asp Leu Glu Asp Leu Lys Ala Ser His Gly Ala Glu Tyr Trp Leu Lys
            180             185             190

Trp Ile Asn Arg Asp Leu Gly Arg Arg Ser Asp Ser Ala His Ala Tyr
        195             200             205

Ile His Pro Thr Met Arg Asn Lys Ser Asn Leu Phe Leu Ile Thr Ser
    210             215             220

Thr Lys Ala Asp Lys Val Ile Ile Glu Asn Gly Val Ala Val Gly Val
225             230             235             240

Arg Thr Val Pro Met Lys Pro Val Glu Thr Lys Asn Pro Pro Ser Arg
            245             250             255

Ile Phe Lys Ala Arg Lys Gln Ile Val Val Ser Cys Gly Thr Ile Ser
            260             265             270

Ser Pro Leu Val Leu Gln Arg Ser Gly Ile Gly Ala Ala His Lys Leu
        275             280             285

Arg Gln Ala Gly Ile Lys Pro Ile Val Asp Leu Pro Gly Val Gly Glu
    290             295             300

Asn Phe Gln Asp His Tyr Cys Phe Phe Thr Pro Tyr Tyr Ser Lys Pro
305             310             315             320

Glu Val Pro Thr Phe Asp Asp Phe Val Arg Gly Asp Pro Val Ala Gln
            325             330             335

Lys Ser Ala Phe Asp Gln Trp Tyr Ser Asn Lys Asp Gly Pro Leu Thr
            340             345             350

Thr Asn Gly Ile Glu Ala Gly Val Lys Ile Arg Pro Thr Asp Glu Glu
        355             360             365

Leu Ala Thr Ala Asp Asp Asp Phe Ile Gln Gly Tyr His Glu Tyr Phe
    370             375             380

Asp Asn Lys Pro Asp Lys Pro Leu Met His Tyr Ser Val Ile Ser Gly
385             390             395             400

Phe Phe Gly Asp His Thr Lys Ile Pro Asn Gly Lys Phe Phe Thr Met
            405             410             415

Phe His Phe Leu Glu Tyr Pro Phe Ser Arg Gly Phe Val Tyr Ala Val
        420             425             430
```

```
Ser Pro Asp Pro Tyr Glu Ala Pro Asp Phe Asp Pro Gly Phe Leu Asn
        435             440             445

Asp Ser Arg Asp Met Trp Pro Met Val Trp Ser Tyr Lys Lys Ser Arg
        450             455             460

Gln Thr Ala Arg Arg Met Glu Ser Phe Ala Gly Glu Val Thr Ser His
465             470             475             480

His Pro Leu Tyr Pro Val Asp Ser Pro Ala Arg Ala Lys Asp Leu Asp
            485             490             495

Leu Glu Thr Cys Lys Ala Phe Ala Gly Pro Asn His Phe Thr Ala Asn
            500             505             510

Leu Tyr His Gly Ser Trp Thr Val Pro Ile Glu Lys Pro Thr Pro Lys
        515             520             525

Asn Asp Ser His Val Thr Cys Asn Gln Val Glu Ile Phe Ser Asp Ile
        530             535             540

Asp Tyr Ser Ala Glu Asp Asp Glu Ala Ile Val Lys Tyr Ile Lys Glu
545             550             555             560

His Thr Glu Thr Thr Trp His Cys Leu Gly Thr Cys Ser Met Ala Pro
            565             570             575

Gln Glu Gly Ser Lys Ile Ala Pro Lys Gly Gly Val Val Asp Ala Arg
        580             585             590

Leu Asn Val Tyr Glu Val Lys Asn Leu Lys Val Ala Asp Leu Ser Ile
        595             600             605

Cys Pro Asp Asn Val Gly Cys Asn Thr Tyr Ser Thr Ala Leu Leu Ile
        610             615             620

Gly Glu Lys Ala Ala Thr Leu Val Ala Glu Asp Leu Gly Tyr Ser Gly
625             630             635             640

Ser Asp Leu Ala Met Thr Ile Pro Asn Phe Lys Leu Gly Thr Tyr Glu
            645             650             655

Glu Lys Gly Leu Ala Arg Phe
            660
```

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<210> 79
<211> 2348
<212> DNA
<213> Ogataea minuta

<400> 79
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aggcgcactt taaaagataa tctacatcca gaaaaataaa aaaataaaac tgaaccggca 120
tttgcgatta cgtaagccac aaaatttcag gaaactcgta caagatcagg ttggcgaggg 180
ggctagcgat agaatgtatc agtgttatta gtggctctag gagtagaaaa caatagaata 240
aagatccgaa gaaagggagc aagaaggcca cgccagacgt tctagtaggt agcccaatcg 300
tcaatgtagc tgttcaggtc tttcaacagg ttcttggtct cgtctggact ggagatccaa 360
```

```
caagtcgttg ctgcggttcg actggcatag tcgttggcgc cgagggagct gaactggtcg 420
ccgacgtgca gggtgttttc gggcttgatg gttcggttgt cgttgcagct gaggaactct 480
tggaggattt tcaccccgta ggacttgtcg ccaatatcga cccagatgtc cgagcctccg 540
ttgaaagcgc accatctgat tttcttagag gaagggaagt ggcggagacg tttgtctacg 600
cgcagaacca cctcttccag ctgctcgcga acgagtttgt agccttcttt ggggaccagt 660
ccaacggcac gctcctttct gatgatgatg gcatgcaatg aaagtttctt gatcaggtcc 720
gagaagatct cctgcgcaaa gtccagggtc cggatgatgt cttcctcgga ccagtcgagc 780
atgtttcaa gcagccattt gtctttggag aagaactcga gtccgccaag ctcgttggag 840
tagcggaata ggtagtttgc ttcgcctccc atcaccagaa cgttctggcg ctgtctgtcg 900
gtgagctttg gggtggtctt cacctcgtct atgagcccct tgagtcgggc gtagtacttg 960
gagccgtcgg agtagcccgc ggcagtgacg atgccgacat agaggtcttt ggcgagcagc 1020
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gagggcgcta caagtctcct tttgctgatt gtgcggcgtc cgtcctcgat gtagaacgcc 1260
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gacatttcag gcattcccgc ctgggtcatc tcgatgttgt cgttgatcag cagctcgagg 1380
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atccactcaa tcagtccgtc tcggcggtgc tccttgagcg cgtactcgac tctgtatctg 1560
gttgtcattt gcgggagggg tgtaaagcag ctcagccggt gactgtgcaa ggacgaacgg 1620
ttcctacttg aatgctaggc tggctaattg ggtatggcac aaacggcaca aacggcagat 1680
gactgcaaat gacgacggta aacagaatcc actcagctgg cactaactgg gtgtagacta 1740
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aaactgcgta taaatagcta cttccatctc ctacttgttg caccattgcc atagtaagaa 2280
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cgaaaaaa                                                           2348
```

<210> 80
<211> 802
<212> DNA
<213> Ogataea minuta

<400> 80
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aatgaaaata gtctacatga atgaaagaga tagctgacca atacggggcg tctggtcacg 180
tgatgtatca cgtgatcttt aagttttcga aatgactaaa tttataacga aaaaaagagt 240
ctaaatgaaa aaaatcgat ctctgccaaa gactcatcga taggctaact caggaagcat 300
tccgagcaac gcataatgcc ctcaaccaca gtctcagaga tgcgcaaaaa ggtgctgatg 360
atcgacaatt acgactcgtt cacatggaac ttgtacgagt atctttgtca agagggagcc 420
gatgtcgagg tctatcgtaa cgacaagatc acaattgaag aaatcgagga aatgaagcct 480
gacattatag tgatttcgcc aggccccgga catccgagat cggactctgg tatctctcga 540
aagactattg agattttcaa gggccggatt cctgtttttg gagtgtgcat gggccaacag 600
tgcatttacg aggttttcgg gggagacgtt gagtacgctg gtgaaattgt tcacggaaaa 660
acctcttctg tgacccacga caatcgtgga gtcttcaaga acgttccgca gggagttgct 720
gtgacgagat accattcgtt ggctggaacg ctaaaaactt tgcccagcga gttggaggtg 780
actgcccgta ccactaacgg ta                                          802
```

```
<210> 81
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAP5 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 81
ctgcagcccc ttctgttttt cttttgacgg                               30


<210> 82
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAP3 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 82
cccccggatc caggaacccg ggaacagaat ctagattttt tcgtaagtcg taagtcgtaa 60
cagaacacaa gagtctttga acaagttgag                               90


<210> 83
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAT5 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 83
ccccccccgga tccgagacgg tgcccgactc ttgttcaatt cttttgg          47


<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer OAT3 for production of an expression
      cassette with AOX1 gene promoter and terminator

<400> 84
cccataatgg taccgttagt ggtacgggca gtc                           33
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<210> 85
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer HGP5 for amplification of a gene conferring
      resistance against hygromycin B

<400> 85
gtcgacatga aaaagcctga actcaccgc                                    29


<210> 86
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer HGP3 for amplification of a gene conferring
      resistance against hygromycin B

<400> 86
actagtctat tcctttgccc tcggacg                                      27


<210> 87
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of 5'-region of
      fi-mannosidase gene

<400> 87
gggggtcga catggtggtc ttcagcaaaa ccgctgccc                          39


<210> 88
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of 5'-region of
      fi-mannosidase gene

<400> 88
ggggggcggc cgcgtgatgt tgaggttgtt gtacggaacc ccc                    43
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<210> 89
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of Saccharomyces
      cerevisiae SUC2 gene

<400> 89
ggggactagt atgcttttgc aagctttcct tttccttttg   40

<210> 90
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer for amplification of Saccharomyces
      cerevisiae SUC2 gene

<400> 90
ccccagatct tattttactt cccttacttg gaacttgtc   39

<210> 91
<211> 711
<212> DNA
<213> Homo sapiens

<400> 91
ctcaccatga gggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgca 60
cgatgtgaca tccagatgac ccagtctcca tcttccgtgt ctgcatctgt aggagacaga 120
gtcaccatca cttgtcgggc gagtcaggtt attagcagct ggttagcctg gtatcagcag 180
aaaccaggga aagcccctaa gctcctgatc tatgctgcat ccagtttgca aagtggggtc 240
ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcaccat cagcagcctg 300
cagcctgaag attttgcaac ttactattgt caacaggcta acagtttccc tccgacgttc 360
ggccaaggga ccaaggtgga aatcaaacgt acggtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgttg a   711

<210> 92
<211> 234
<212> PRT
<213> Homo sapiens

<400> 92
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
  1   5   10   15

Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser
              20   25   30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val
         35   40   45

Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    50   55   60

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
65   70   75   80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
             85   90   95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
             100   105   110

Ser Phe Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
         115   120   125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130   135   140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145   150   155   160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
             165   170   175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
             180   185   190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
    195   200   205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210   215   220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230

<210> 93
<211> 1428
<212> DNA
<213> Homo sapiens

<400> 93
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tgtgcagcct ctggattcac cttcagtagc tatagcatga actgggtccg ccaggctcca 180
gggaaggggc tggagtgggt ctcatccatt agtagtagta gtagttacat atactacgca 240
gactcagtga agggccgatt caccatctcc agagacaacg ccaagaactc actgtatctg 300
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag agatcggatt 360
attatggttc ggggagtcta ctactactac ggtatggacg tctggggcca agggaccacg 420
gtcaccgtct cctcagctag caccaagggc ccatcggtct tccccctggc accctcctcc 480
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 540

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ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 600
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc 660
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 720
aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct 780
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg 840
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accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg 1320
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg 1380
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatga        1428
```

<210> 94
<211> 475
<212> PRT
<213> Homo sapiens

<400> 94

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Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
  1               5                  10                  15

Val Gln Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
             20                  25                  30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
         35          .          40                  45

Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
     50                  55                  60

Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala
 65                  70                  75                  80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                 85                  90                  95

Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
             100                 105                 110

Tyr Tyr Cys Ala Arg Asp Arg Ile Ile Met Val Arg Gly Val Tyr Tyr
         115                 120                 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
     130                 135                 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145                 150                 155                 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
                 165                 170                 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
             180                 185                 190
```

```
Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
        195             200             205

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
    210             215             220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225             230             235             240

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
            245             250             255

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
        260             265             270

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        275             280             285

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    290             295             300

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
305             310             315             320

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            325             330             335

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
            340             345             350

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
    355             360             365

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    370             375             380

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
385             390             395             400

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
            405             410             415

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        420             425             430

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        435             440             445

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    450             455             460

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465             470             475
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<210> 95
<211> 7
<212> PRT
<213> Saccharomyces cerevisiae

<400> 95
Val Gly Phe Leu Asp His Met
　1　　　　　　　　　　5

<210> 96
<211> 7
<212> PRT
<213> Saccharomyces cerevisiae

<400> 96
Pro Ser Thr Lys Gly Val Leu
　1　　　　　　　　　　5

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
　　　primer PHI5 for amplification of Ogataea minuta
　　　HIS3 gene

<220>
<221> modified_base
<222> (2)
<223> a, c, g or t

<220>
<221> modified_base
<222> (5)
<223> a, c, g or t

<220>
<221> modified_base
<222> (11)
<223> a, c, g or t

<400> 97
tnggnttyyt ngaycayatg   20

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
　　　primer PHI3 for amplification of Ogataea minuta
　　　HIS3 gene

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<222> (3)
<223> a, c, g or t

<220>
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<222> (6)
<223> a, c, g or t

<220>
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<222> (12)
<223> a, c, g or t

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<221> modified_base
<222> (15)
<223> a, c, g or t

<220>
<221> modified_base
<222> (18)
<223> a, c, g or t

<400> 98
arnacnccyt tngtnswngg                                              20


<210> 99
<211> 3831
<212> DNA
<213> Ogataea minuta

<400> 99
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ccagtgaaga tatccgggac ggttggaaca gctctttat caacaagaaa tctgagattg 180
aggaaccagc gtccaacaca aaaagcgact ctgcttcgtc tgtcaagaag accaaggcga 240
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acctgcttaa atcgatcaag tttcttgaga gacatctata catagtgagc gagcagcaga 420
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atcacattgt ttccagatgc gagattatca agcaagaaca cgaacaagag ggccaagaag 720
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tcaacctgcc ttcccagaaa accccggagt acgaggcttt caagcaacta ccggagccaa 840
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tcattgcttg cagttttttg agaatctcag agttcttcca cttctcaggc agcggggtga 1260
cgtcgtactt cttagtggcc caatagtaga tatcccagtc cggctcatca agcaatttgt 1320
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ggaaagcagc gacagatcgg ccgaccgcga ctatcgacgc gacgataggg attttttttt 1740
ttaaaaaaaa gagtcaaaaa aacatcctga agagaaactt ttcatgggga accatgtcca 1800
ggagtcatcc gacggtatcc ctttacagtc aaaaaaacat gtctgaagag aacaagaaac 1860
gcaagctgga aaacggcaca aatgatgcaa aagctgctcg gtttgcagag gtgagaagag 1920
tcaccaatga aaccagcatc cagatcatcc tgaacttgga tggtggactc atcgagtgca 1980
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<211> 238
<212> PRT
<213> Ogataea minuta

<400> 100

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Ser Ile Gln Ile Ile Leu Asn Leu Asp Gly Gly Leu Ile Glu Cys Lys
        35                  40                  45
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Asn Thr Ser Ala Gln Val Ile Ser Ile Lys Thr Gly Leu Gly Phe Leu
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Asp His Met Leu His Ala Leu Ala Lys His Ser Gly Trp Ser Leu Ile
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Val Glu Cys Ile Gly Asp Leu His Ile Asp Asp His His Thr Ala Glu
            100             105             110

Asp Val Gly Ile Ala Leu Gly Glu Thr Phe Lys Arg Ala Leu Gly Pro
            115             120             125

Val Lys Gly Leu Lys Arg Phe Gly His Ala Tyr Ala Pro Leu Asp Glu
    130             135             140

Ala Leu Ser Arg Ala Val Val Asp Leu Ser Asn Arg Pro Phe Ala Val
145             150             155             160

Val Glu Leu Gly Leu Arg Arg Glu Lys Ile Gly Asp Leu Ser Cys Glu
            165             170             175

Met Ile Pro His Val Leu Glu Ser Phe Ala Thr Ser Ala His Ile Thr
            180             185             190

Met His Val Asp Cys Leu Arg Gly Phe Asn Asp His His Arg Ser Glu
            195             200             205

Ser Ala Phe Lys Ala Leu Ala Val Ala Ile Arg Asp Ala Thr Ser Tyr
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Thr Gly Arg Asp Asp Val Pro Ser Thr Lys Gly Val Leu Met
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<210> 101
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer DHI5

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<210> 102
<211> 21
<212> DNA
<213> Artificial Sequence

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<210> 103
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<212> PRT
<213> Saccharomyces cerevisiae

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<210> 104
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 104
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<210> 105
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
      primer PLE5 for amplification of Ogataea minuta
      LEU2 gene

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<220>
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<400> 105
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<210> 106
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<220>
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      primer PLE3 for amplification of Ogataea minuta
      LEU2 gene

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<400> 106
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<210> 107
<211> 5615
<212> DNA
<213> Ogataea minuta

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<210> 108
<211> 363
<212> PRT
<213> Ogataea minuta

<400> 108
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Lys Pro Glu Ile Lys Phe Asn Phe Glu His His Leu Ile Gly Gly Ala
            35                  40                  45

Ala Ile Asp Ala Thr Gly Gln Pro Ile Thr Asp Ala Ala Leu Glu Ala
        50                  55                  60

Ser Lys Lys Ala Asp Ala Val Leu Leu Gly Ser Val Gly Gly Pro Lys
65                  70                  75                  80

Trp Gly Thr Gly Gln Val Arg Pro Glu Gln Gly Leu Leu Lys Ile Arg
                85                  90                  95

Lys Glu Leu Asn Leu Tyr Ala Asn Leu Arg Pro Cys Ser Phe Ala Ser
                100                 105                 110

Asp Ala Leu Leu Asp Leu Ser Pro Leu Lys Pro Glu Ile Val Arg Gly
            115                 120                 125
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Thr Asp Phe Val Val Val Arg Glu Leu Val Gly Gly Ile Tyr Phe Gly
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Glu Arg Lys Glu Asp Asp Gly Ser Gly Phe Ala Ser Asp Thr Glu Ala
145   150   155   160

Tyr Ser Val Pro Glu Val Gln Arg Ile Thr Arg Met Ala Ala Phe Met
          165   170   175

Ala Leu Gln Ser Asp Pro Pro Leu Pro Val Tyr Ser Leu Asp Lys Ala
        180   185   190

Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu Thr
        195   200   205

Ile Lys Asn Glu Phe Pro Gln Leu Lys Leu Gln His His Leu Ile Asp
    210   215   220

Ser Ala Ala Met Ile Leu Val Lys Ser Pro Thr Lys Leu Asn Gly Val
225   230   235   240

Val Leu Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala Ser
        245   250   255

Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala Ser
        260   265   270

Leu Pro Asp Ser Asn Glu Ala Phe Gly Leu Tyr Glu Pro Cys His Gly
        275   280   285

Ser Ala Pro Asp Leu Ala Lys Gly Leu Val Asn Pro Leu Ala Thr Ile
    290   295   300

Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Leu Val Glu Glu
305   310   315   320

Gly Arg Ala Val Glu Lys Ala Val Arg Ala Val Leu Asp Gln Gly Ile
        325   330   335

Met Thr Ala Asp Leu Gly Gly Ser Ser Ser Thr Thr Glu Val Gly Asp
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Ala Val Ala Lys Glu Val Thr Lys Leu Leu Gly
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<210> 109
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
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<210> 110
<211> 20
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<220>
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<210> 111
<211> 8
<212> PRT
<213> Saccharomyces cerevisiae

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<210> 112
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<212> PRT
<213> Saccharomyces cerevisiae

<400> 112
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<210> 113
<211> 24
<212> DNA
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<220>
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      primer PLE5 for amplification of Ogataea minuta YPS1 gene

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<400> 113
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<210> 114
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ttygghgcna tygaycaygc naa                                               23


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<212> DNA
<213> Ogataea minuta

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<213> Ogataea minuta

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             20   25   30

Glu Ile Tyr Arg Gly His Ser Phe Glu Thr Ser Gln Arg Gly Gly Arg
        35   40   45

Pro Tyr Met Leu Glu Lys Arg Ala Glu Asp Gly Ser Val Leu Met Glu
        50   55   60

Leu Gln Asn Asn Gln Ser Phe Tyr Lys Val Glu Leu Glu Val Gly Ser
65   70   75   80

Asp Lys Gln Lys Ile Gly Val Leu Val Asp Thr Gly Ser Ser Asp Leu
            85   90   95

Trp Ile Met Asn Gln Asn Asn Ser Tyr Cys Glu Ser Ser Ser Ser Ser
        100   105   110

Ser Lys Met Arg Glu Arg Lys Gly Arg Lys Leu Ser Asp Leu Arg Asn
        115   120   125

Leu Asn Leu Asp Val Ser Glu Lys Asn Val Lys Ala Val Gly Ala Ala
    130   135   140

Glu Thr Glu Thr Met Thr Leu Ser Val Gly Glu Gly Leu Phe Ser Trp
145   150   155   160

Phe Glu Thr Gln Thr Asp Gly Ser Gly Gly Glu Thr Glu Thr Ala Ser
            165   170   175

Gly Asp Ser Ser Glu Ala Thr Ile Asp Cys Ser Val Tyr Gly Thr Phe
        180   185   190

Asp Pro Ser Ser Ser Asp Thr Phe Lys Ser Asn Gly Thr Glu Phe Ser
        195   200   205

Ile Ser Tyr Ala Asp Asp Ser Phe Ala Lys Gly Thr Trp Gly Thr Asp
    210   215   220

Asp Val Thr Phe Asn Gly Val Thr Val Asp Gln Leu Ser Met Ala Ile
225   230   235   240

Ala Asp Glu Thr Asn Ser Ser Met Gly Val Leu Gly Ile Gly Leu Lys
            245   250   255

Gly Leu Glu Thr Thr Tyr Ser Gly Asp Val Thr Asn Ala Tyr Thr Tyr
        260   265   270

Glu Asn Leu Pro Tyr Lys Met Gln Ser Gln Gly Leu Ile Ser Lys Pro
        275   280   285

Val Tyr Ser Val Tyr Leu Asn Asp Ser Glu Ser Ser Ala Ala Ser Ile
    290   295   300

Leu Phe Gly Ala Val Asp His Asp Lys Tyr Thr Gly Thr Leu Thr Leu
305   310   315   320

Leu Pro Ile Ile Asn Thr Ala Glu Ser Leu Gly Tyr Ser Thr Pro Val
            325   330   335

Arg Leu Glu Val Thr Leu Ser Lys Leu Tyr Thr Gly Ser Ser Ser Asn
        340   345   350

Lys Thr Ala Val Ser Ile Ala Ser Gly Ala Ala Ala Ala Leu Leu Asp
        355   360   365

Thr Gly Thr Thr Leu Thr Tyr Val Pro Ser Asp Ile Ile Ser Thr Ile
    370   375   380

Val Asp Gln Tyr Gly Phe Gln Tyr Ser Ser Ser Val Gly Thr Tyr Val
385   390   395   400

Ala Lys Cys Asp Ser Leu Asp Asp Ala Glu Ile Val Phe Asp Phe Gln
            405   410   415

Gly Thr Lys Ile Trp Val Pro Phe Ser Ser Phe Ala Val Ser Leu Thr
            420   425   430

Thr Asn Gly Gly Ser Gln Ser Ser Tyr Cys Ala Leu Gly Leu Met Asp
        435   440   445

Ser Gly Asp Asp Thr Phe Thr Leu Gly Asp Ser Phe Leu Asn Asn Val
    450   455   460

Tyr Phe Val Ala Asp Leu Glu Asn Leu Gln Ile Ala Ile Ala Pro Ala
465   470   475   480

Asn Leu Asp Ser Thr Ser Glu Asp Ile Glu Val Val Ser Asp Ser Gly
            485   490   495

Ile Pro Ser Ala Lys Ser Ala Ser Ala Tyr Ser Ser Ser Trp Gly Ala
            500   505   510

Ser Gly Ser Ala Val Ala Ser Ser Leu Ser Val Gln Thr Gly Ala Glu
        515   520   525

Thr Val Thr Ser Thr Asp Ala Gly Ser Asp Ser Thr Gly Ser Ala Ser
    530   535   540

Gly Ser Ser Gly Ser Ala Ser Ser Ser Ser Ser Lys Ser Ser Ala Ser
545   550   555   560

Ser Ser Ser Gly Ser Ser Gly Ser Ser Ser Lys Ser Gly Ser Ser Ser
            565   570   575

Ser Lys Tyr Ala Ala Gly Asn Ala Trp Gly Met Ser Val Cys Ser Leu
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Ala Phe Thr Ile Ala Val Ser Val Leu Val Ile Gly
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